



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Margolis, Benjamin L.
- (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATMENT OF BREAST CANCER
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: PENNIE & EDMONDS
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/207,575
 - (B) FILING DATE: 07-MAR-1994
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Coruzzi, Laura A.
 - (B) REGISTRATION NUMBER: 30,742
 - (C) REFERENCE/DOCKET NUMBER: 7683-053
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 790-9090
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 - (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gly	Xaa	Gly	Xaa	Xaa	Gly
1					5

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Ala Val Lys
1

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Met Xaa Tyr Leu
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ile His Arg Asp Leu Ala Ala Arg Asn
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys Trp Met Ala Pro Glu
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Trp Thr Ala Pro Glu
1 5

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Phe Trp Tyr Ala Pro Glu
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Asp Val Trp Ser Phe Gly
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Arg Asp Ser Ser Arg Leu Cys Val Val Lys Val Tyr Ser Glu Asp Gly
1 5 10 15

Ala Cys Arg Ser Val Glu Val Ala Ala Gly Ala Thr Ala Arg His Val
20 25 30

Cys Glu Met Leu Val Gln Arg Ala His Ala Leu Ser Asp Glu Ser Trp
35 40 45

Gly Leu Val Glu Ser His Pro Tyr Leu Ala Leu Glu Arg Gly Leu Glu
50 55 60

Asp His Glu Phe Val Val Glu Val Gln Glu Ala Trp Pro Val Gly Gly
65 70 75 80

Asp Ser Arg Phe Ile Phe Arg Lys Asn Phe Ala Lys Tyr Glu Leu Phe
85 90 95

Lys Ser Pro Pro His Thr Leu Phe Pro Glu Lys Met Val Ser Ser Cys

100					105					110					
Leu	Asp	Ala	Gln	Thr	Gly	Ile	Ser	His	Glu	Asp	Leu	Ile	Gln	Asn	Phe
		115					120					125			
Leu	Asn	Ala	Gly	Ser	Phe	Pro	Glu	Ile	Gln	Gly	Phe	Leu	Gln	Leu	Arg
	130					135					140				
Gly	Ser	Gly	Arg	Gly	Ser	Gly	Arg	Lys	Leu	Trp	Lys	Arg	Phe	Phe	Cys
145					150					155					160
Phe	Leu	Arg	Arg	Ser	Gly	Leu	Tyr	Tyr	Ser	Thr	Lys	Gly	Thr	Ser	Lys
				165					170					175	
Asp	Pro	Arg	His	Leu	Gln	Tyr	Val	Ala	Asp	Val	Asn	Glu	Ser	Asn	Val
			180					185					190		
Tyr	Val	Val	Thr	Gln	Gly	Arg	Lys	Leu	Tyr	Gly	Met	Pro	Thr	Asp	Phe
	195						200					205			
Gly	Phe	Cys	Val	Lys	Pro	Asn	Lys	Leu	Arg	Asn	Gly	His	Lys	Gly	Leu
	210					215					220				
His	Ile	Phe	Cys	Ser	Glu	Asp	Glu	Gln	Ser	Arg	Thr	Cys	Trp	Leu	Ala
225					230					235					240
Ala	Phe	Arg	Leu	Phe	Lys	Tyr	Gly	Val	Gln	Leu	Tyr	Lys	Asn	Tyr	Gln
				245					250					255	
Gln	Ala	Gln	Ser	Arg	His	Leu	Arg	Leu	Ser	Tyr	Leu	Gly	Ser	Pro	Pro
			260					265					270		
Leu	Arg	Ser	Val	Ser	Asp	Asn	Thr	Leu	Val	Ala	Met	Asp	Phe	Ser	Gly
		275					280					285			
His	Ala	Gly	Arg	Val	Ile	Asp	Asn	Pro	Arg	Glu	Ala	Leu	Ser	Ala	Ala
	290					295					300				
Met	Glu	Glu	Ala	Gln	Ala	Trp	Arg	Lys	Lys	Thr	Asn	His	Arg	Leu	Ser
305					310					315					320
Leu	Pro	Thr	Thr	Cys	Ser	Gly	Ser	Ser	Leu	Ser	Ala	Ala	Ile		
				325					330						

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys	Glu	Ala	Lys	Val	Thr	Lys	Ile	Phe	Val	Lys	Phe	Phe	Val	Glu	Asp
1				5					10					15	
Gly	Glu	Ala	Leu	Gln	Leu	Leu	Ile	Asp	Glu	Arg	Trp	Thr	Val	Ala	Asp
			20					25					30		
Thr	Leu	Lys	Gln	Leu	Ala	Glu	Lys	Asn	His	Ile	Ala	Leu	Met	Glu	Asp
		35					40					45			
His	Cys	Ile	Val	Glu	Glu	Tyr	Pro	Glu	Leu	Tyr	Ile	Lys	Arg	Val	Tyr

50					55					60					
Glu 65	Asp	His	Glu	Lys	Val 70	Val	Glu	Asn	Ile	Gln 75	Met	Trp	Val	Gln	Asp 80
Ser	Pro	Asn	Lys	Leu 85	Tyr	Phe	Met	Arg	Arg 90	Pro	Asp	Lys	Tyr	Ala 95	Phe
Ile	Ser	Arg	Pro 100	Glu	Leu	Tyr	Leu	Leu 105	Thr	Pro	Lys	Thr	Ser 110	Asp	His
Met	Glu	Ile 115	Pro	Ser	Gly	Asp	Gln 120	Trp	Thr	Ile	Asp	Val 125	Lys	Gln	Lys
Phe	Val 130	Ser	Glu	Tyr	Phe	His 135	Arg	Glu	Pro	Val	Val 140	Pro	Pro	Glu	Met
Glu 145	Gly	Phe	Leu	Tyr	Leu 150	Lys	Ser	Asp	Gly	Arg 155	Lys	Ser	Trp	Lys	Lys 160
His	Tyr	Phe	Val	Leu 165	Arg	Pro	Ser	Gly	Leu 170	Tyr	Tyr	Ala	Pro	Lys 175	Ser
Lys	Lys	Pro	Thr 180	Thr	Lys	Asp	Leu	Thr 185	Cys	Leu	Met	Asn	Leu 190	His	Ser
Asn	Gln	Val 195	Tyr	Thr	Gly	Ile	Gly 200	Trp	Glu	Lys	Lys	Tyr 205	Lys	Ser	Pro
Thr 210	Pro	Trp	Cys	Ile	Ser	Ile 215	Lys	Leu	Thr	Ala	Leu 220	Gln	Met	Lys	Arg
Ser 225	Gln	Phe	Ile	Lys	Tyr 230	Ile	Cys	Ala	Glu	Asp 235	Glu	Met	Thr	Phe	Lys 240
Lys	Trp	Leu	Val	Ala 245	Leu	Arg	Ile	Ala	Lys 250	Asn	Gly	Ala	Glu	Leu 255	Leu
Glu	Asn	Tyr	Glu 260	Arg	Ala	Cys	Gln	Ile 265	Arg	Arg	Glu	Thr	Leu 270	Gly	Pro
Ala	Ser	Ser 275	Met	Ser	Ala	Ala	Ser 280	Ser	Ser	Thr	Ala	Ile 285	Ser	Glu	Val
Pro	His 290	Ser	Leu	Ser	His	His 295	Gln	Arg	Thr	Pro	Ser 300	Val	Ala	Ser	Ser
Ile 305	Gln	Leu	Ser	Ser	His 310	Met	Met	Asn	Asn	Pro 315	Thr	His	Pro	Leu	Ser 320
Val	Asn	Val	Arg	Asn 325	Gln	Ser	Pro	Ala	Ser 330	Phe	Ser	Val	Asn	Ser 335	Cys
Gln	Gln	Ser	His 340	Pro	Ser	Arg	Thr	Ser 345	Ala	Lys	Leu				

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1, 25-27, 32, 46, 47, 49, 52, 54, 72
75, 77, 93, 95, 105, 107, 108 and 111
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Hydrophobic
residues"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2, 21, 23 and 101
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Basic residues"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3, 7, 9, 11-19, 22, 28-31, 36-42, 44, 48
50, 51, 53, 55-70, 74, 76, 78-90, 92, 94
96-98, 106 109 and 110
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Non-consensus
residues"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 24, 33-35 and 91
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Aromatic
residues"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 99, 100, 102 and 103
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Acidic residues"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Xaa	Xaa	Xaa	Gly	Phe	Leu	Xaa	Lys	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	1	5	10	15
Xaa	Xaa	Xaa	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	20	25	30	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Gly	Xaa	Xaa	Xaa	35	40	45	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	50	55	60	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	65	70	75	80
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	85	90	95	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	100	105	110	

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Isoleucine or Valine"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2, 69 and 102
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Arginine or Lysine"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Tyrosine or Tryptophan"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7, 11-17, 22, 28, 29, 31, 33, 35, 38-42
46, 47, 50-52, 58-68, 70, 72, 74, 76-78
80-92, 96, 98, 109, 110
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Non-consensus residues"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8, 9, 18 and 21
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Lysine or Arginine"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Threonine or Serine"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 24
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Tryptophan or Tyrosine"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 26 and 57
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Valine or Isoleucine"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 30
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Aspartic Acid or Glycine"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 34
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Leucine or Tyrosine"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 36
 - (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Tyrosine or Phenylalanine"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 37
 - (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Lysine or Glutamic Acid"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 55
 - (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Cysteine or Valine"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 56
 - (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Glutamine or Glutamic Acid"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 71
 - (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Asparagine or Histidine"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 75 and 108
 - (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Isoleucine
or Leucine"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 93
 - (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Phenylalanine or Leucine"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 94
 - (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Glutamine or Alanine"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 97
 - (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Serine or Threonine"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 102 and 103
 - (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Glutamic Acid
or Aspartic Acid"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 105
 - (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Valine or Methionine"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 111
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Alanine or Valine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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Ile Arg Glu Gly Tyr Leu Xaa Lys Lys Gly Xaa Xaa Xaa Xaa Xaa Xaa
1          5          10          15
Xaa Lys Thr Trp Lys Xaa Arg Trp Phe Val Leu Xaa Xaa Asp Xaa Leu
20          25          30
Xaa Leu Xaa Tyr Lys Xaa Xaa Xaa Xaa Xaa Pro Lys Gly Xaa Xaa Pro
35          40          45
Leu Xaa Xaa Xaa Ser Val Cys Gln Val Xaa Xaa Xaa Xaa Xaa Xaa
50          55          60
Xaa Xaa Xaa Xaa Arg Xaa Asn Xaa Phe Xaa Ile Xaa Xaa Xaa Asp Xaa
65          70          75          80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Gln Ala Xaa
85          90          95
Ser Xaa Glu Glu Arg Glu Glu Trp Val Lys Ala Ile Xaa Xaa Ala
100         105         110

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Asp Leu Arg Ala Ala Asn
1          5

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Isoleucine or Valine"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Lysine or Arginine"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /label= Xaa
 /note= "Xaa = Threonine or Methionine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro Xaa Xaa Trp Xaa Ala Pro Glu
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /label= Xaa
 /note= "Xaa = Valine or Isoleucine"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 7
 (D) OTHER INFORMATION: /label= Xaa
 /note= "Xaa = Valine or Isoleucine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Xaa Pro Xaa Tyr Xaa Asn Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 8
 (D) OTHER INFORMATION: /label= Xaa
 /note= "Xaa = Hydrophobic Residue"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Xaa Pro Xaa Xaa Pro Pro Pro Xaa Xaa Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Pro Val Pro Pro Arg Arg
1 5